

IN THE CLAIMS

In accordance with the revised format for claim amendments, all claims are shown below. Please amend the claims as follows:

1. (Currently Amended) A nucleic acid molecule having a nucleic acid sequence that encodes a linker region of exoglucanase, said nucleic acid sequence comprising the nucleotide sequence: of SEQ ID NO: 3 ~~5'-GGCGGAAACCCGCCTGGCACCACC-3'~~.
2. (Original) The nucleic acid molecule of claim 1 wherein said exoglucanase is further defined as a cellobiohydrolase.
3. (Original) The nucleic acid molecule of claim 1 wherein said exoglucanase is further defined as a 1,4- $\beta$ -cellobiohydrolase.
4. (Currently Amended) The nucleic acid molecule of claim 1 whereas said nucleic acid sequence is further defined as comprising SEQ ID NO: 19.
5. (Cancelled) ~~CCTCCCCGGCGGAAACCCGCCTGGCACCACCACCACCCGCGGCCCA-3'~~.
6. (Original) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase, said nucleic acid sequence comprising a linker region sequence having a length of from about 20 nucleotides to about 50 nucleotides linker region, between a catalytic domain and a cellulose binding domain (CBD).
7. (Original) The nucleic acid molecule of claim 5 wherein the variant cellobiohydrolase is further defined as having enhanced thermostability.
8. (Original) The nucleic acid molecule of claim 5 wherein the variant cellobiohydrolase is further defined as an 1,4  $\beta$ -cellobiohydrolase.
9. (Original) The nucleic acid molecule of claim 5 wherein the cellobiohydrolase is further defined as having reduced end-product inhibition.
10. (Original) The nucleic acid molecular of claim 5 wherein the linker region sequence has a length of about 24 nucleotides.
11. (Original) A method for making an active exoglucanase in a eukaryotic heterologous host, the method comprising reducing glycosylation of the exoglucanase, wherein reducing comprises replacing an N-glycosylation site amino acid residue with non-glycosyl accepting amino acid residue.

12. (Original) The method of claim 10, wherein the N-glycosylation site amino acid residues include asparagines 45, 270, or 384 of Table 4 and the non-glycosyl accepting amino acid residue includes alanine.
13. (Original) The method of claims 10, wherein replacing comprises site-directed mutagenesis.
14. (Original) The methods of claims 10, wherein the exoglucanase comprises a cellobiohydrolase.
15. (Currently Amended) An exoglucanase, comprising of the sequence change of Table 4, N45A, 5'-GGACTCACGCTACGGCCCAGCAGCACGAACTGC 3' SEQ ID NO: 20.
16. (Currently Amended) An exoglucanase, comprising of the sequence change of Table 4, N270A, 5'-CCCATAACCGCCTGGGGCCCACCAGCTTCTACGGCCC 3' SEQ ID NO: 21.
17. (Currently Amended) An exoglucanase, comprising of the sequence change of Table 4, N384A, 5'-GGACTCCACCTACCCGACAGCCCGAGACCTCCTCCACACCCG 3' SEQ ID NO: 22.
18. (Currently Amended) An exoglucanase, comprising a combination of claims 14,15,16,17.

IN THE FIGURES

Figure 1. Coding sequence for the *cbh1* gene (SEQ ID NO: 4). Small case letters represent the signal sequence, large case letters the catalytic domain, bolded italics the linker region, and large case underlined the cellulose-binding domain.

atgtatcggaagttggcgcgtcatctggccttcttggccacagctcgtgctCAGTCGGCCTGCACTCTCCAATCGGAACTCAC  
CCGCCTCTGACATGGCAGAAATGCTCGTCTGGTGGCACGTGCACTCAACAGACAGGCTCCGTG  
GTCATCGACGCCAACTGGCGCTGGACTCACGCTACGAACAGCAGCACGAACTGCTACGATGG  
CAACACTTGGAGCTCGACCCTATGTCCTGACAACGAGACCTGCGCGAAGAAGTGTGTCTGGA  
CGGTGCCGCCTACGCGTCCACGTACGGAGTTACCACGAGCGGTAACAGCCTCTCCATTGGCTT  
TGTCACCCAGTCTGCGCAGAAGAACGTTGGCGCTCGCCTTTACCTTATGGCGAGCGACACGAC  
CTACCAGGAATTCACCCTGCTTGGCAACGAGTTCTCTTTTCGATGTTGATGTTTTCGAGCTGCCG  
TGCGGCTTGAACGGAGCTCTCTACTTCGTGTCCATGGACGCGGATGGTGGCGTGAGCAAGTAT  
CCCACCAACACCGCTGGCGCCAAGTACGGCACGGGGTACTGTGACAGCCAGTGTCCTCCGCGA  
TCTGAAGTTCATCAATGGCCAGGCCAACGTTGAGGGCTGGGAGCCGTCATCCAACAACGCGA  
ACACGGGCATTGGAGGACACGGAAGCTGCTGCTCTGAGATGGATATCTGGGAGGCCAACTCC  
ATCTCCGAGGCTCTTACCCCCCACCCTTGACGACTGTCGGCCAGGAGATCTGCGAGGGTGAT  
GGGTGCGGCGGAACCTACTCCGATAACAGATATGGCGGCACCTTTCGATCCCGATGGCTGCGA  
CTGGAACCCATACCGCCTGGGCAACACCAGCTTCTACGGCCCTGGCTCAAGCTTTACCCTCGA  
TACCACCAAGAAATTGACCGTTGTCACCCAGTTTCGAGACGTCGGGTGCCATCAACCGATACTA  
TGTCCAGAATGGCGTCACTTTCCAGCAGCCCAACGCCGAGCTTGGTAGTTACTCTGGCAACGA  
GCTCAACGATGATTACTGCACAGCTGAGGAGGCAGAATTCGGCGGATCCTCTTTCTCAGACAA  
GGGCGGCCTGACTCAGTTCAAGAAGGCTACCTCTGGCGGCATGGTTCTGGTCATGAGTCTGTG  
GGATGATTACTACGCCAACATGCTGTGGCTGGACTCCACCTACCCGACAAACGAGACCTCCTC  
CACACCCGGTGCCGTGCGCGGAAGCTGCTCCACCAGCTCCGGTGTCCCTGCTCAGGTGCAATC  
TCAGTCTCCCAACGCCAAGGTCACCTTCTCCAACATCAAGTTTCGGACCCATTGGCAGCACCGG  
CAACCCTAGCGGCGGCAAC***CTCCCGGCGGAACCCGCTGGCACCAACCACCACCCGCCGCC***  
***AGCCACTACCACTGGAAGCTCTCCCGGACCTACCCAGTCTCACTACGGCCAGTGCGGCGGTATT***  
***GGCTACAGCGGCCCCACGGTCTGCGCCAGCGGCACAACCTGCCAGGTCCTGAACCCTTACTAC***  
***TCTCAGTGCCTGTAAAGCTCC***

Figure 4. Coding sequence, SEQ ID NO: 19, for the linker region of the *cbh1* gene, SEQ ID NO: 4, showing additional proline nucleotides that effect conformation of the linker region in the protein structure.

